SEQUENCE LISTING

<110> OLSON, ERIC
FREY, NORBERT

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SPECIFIC
CALCINEURIN ASSOCIATED PROTEIN (CAP)

<130> UTSD:729US

<140> UNKNOWN
<141> 2001-11-07

<150> 60/246,629
<151> 2000-11-07

<160> 12

<170> PatentIn Ver. 2.1

<210> 1
<211> 2531
<212> DNA
<213> Homo sapiens

<400> 1
gtcccaggtt caaggataaa aaccatcagg cccaagtgcc atccatagtc catctccaga 60
gtcttcctcc acaaactggg attcatcccc gctgaaaaag cacaatctaa cagcaaggga 120
acaaaaaaac catgctatca cataatacta tgatgaagca gagaaaacag caagcaacag 180
ccatcatgaa ggaagtccat ggaaatgatg ttgatggcat ggacctgggc aaaaaggtca 240
gcatccccag agacatcatg ttggaagaat tatcccatct cagtaaccgt ggtgccaggc 300
tatttaagat gcgtcaaaga agatctgaca aatacacatt tgaaaatttc cagtatcaat 360
ctagagcaca aataaatcac agtattgcta tgcagaatgg gaaagtggat ggaagtaact 420
tggaaggtgg ttcgcagcaa gccccettga ctcctcccaa caccccagat ccacgaagcc 480
ctccaaatcc agacaacatt gctccaggat attctggacc actgaaggaa attcctcctg 540
aaaaattcaa caccacagct gtccctaagt actatcaatc tccctgggag caagccatta 600
gcaatgatcc ggagctttta gaggctttat atcctaaact tttcaagcct gaaggaaagg 660
cagaactgcc tgattacagg agctttaaca gggttgccac accatttgga ggttttgaaa 720
aagcatcaag aatggttaaa tttaaagttc cagattttga gctactattg ctaacagatc 780
ccaggtttat gtcctttgtc aatccccttt ctggcagacg gtcctttaat aggactccta 840
agggatggat atctgagaat attcctatag tgataacaac cgaacctaca gatgatacca 900
ctgtaccaga atcagaagac ctatgaaaag aaagttgtat gtgccacata aaactctgaa 960
tataaaagtt gctgttctac tattttaact actggcaaag cacttgcatt tttcattagt 1020
agcaacaata gcaatttagt gattttcctt ttctgacatt caatttcaat ctcagatcaa 1080
atactaataa acaattagaa atcttacttt aaaaaactta taactcactt gtcttcattc 1140
ataattttgt tttcacctgg tttaaagaat ccagatattt tactgcaaaa gttcagatgg 1200
aaaagtaatt gacagcttca cctttgtctc attttatatg atttattaca gtgtaagttt 1260
ttcaagtgga atctagaatc aaaatacagg gagagatatg aagacctatt cagagtttca 1320
tctggggatg aaagctatgg aagatgatgt acaaatgtta ttgatggaga aaatggttgg 1380
tgtgtccttt ctggtgacca tgagaaaata atatgtcttg atgaagtctt ttcattagtc 1440
actcttagaa ttctaaagtg ctttgcactt ttcaatatgt tttgaatcat taggtaattt 1500
attctggatg atattctcca aaattcaatt cagttattat attcatttag cattaagtca 1560
aggagactga gaatgactca agggacgtca tagtaccata gttttaagga ccaaggtgtg 1620

```
cccagaattc aagtttcaca aatcccaatg ctgtgcattg attatgttca actttatgtg 1680
tgcattctta gaagagtaag aacaaataaa gtacaccgta atatacatat aaatacattc 1740
atgtttgtga gagaaggaaa gagtaagtaa tttgaattgg cagctttctt tgctaaatct 1800
ttaaattctg ttaagatcct caagtaactg gggagtacat gctttaggac acaaacaaaa 1860
acaaagggca tgaaagtatc tgaaagcaat gtagcacata tctatcgtaa tatatgtaat 1920
atattgacat aaaagacaca aactaatata aagttatagt tatatcttaa aatataattg 1980
aagaagcata tgacatataa cttatagaaa tcagtatcaa ttcctcccat ttcaattcag 2040
ttaagactct gtgatagatg tttatagcag agaagaaatg tctcatcaat aggaaaacta 2100
tcagataaag tttaggagat aggaagaagg actgtgtgta gtaatgaaaa taccaagttg 2160
caacattaca tgtttacaaa aaaaatctgt gtttgtagtg tggaagttgg tgactgtttt 2220
aatcatcatc tagacttgtt aagtagaaaa attttaaaaa tttgcttatg aaaatataac 2280
ccccagaaag taacaatgac aaagtattat atttatatat attattgtag agaatttgta 2340
tatttttaaa gatgtcttaa gatatcttaa ttttatttat aagttttggt gtttacctgt 2400
tttaaaatga taatgttggc atctgtgata aactatcaat gaggctccca tcatgccatt 2460
ttttgttcat tttaatcttt aaaaaataaa aattaggcat attaaaaaaa aaaaaaaaaa 2520
aaaaaaaaaa a                                                      2531


<210> 2
<211> 264
<212> PRT
<213> Homo sapiens

<400> 2
Met Leu Ser His Asn Thr Met Met Lys Gln Arg Lys Gln Gln Ala Thr
 1               5                  10                  15

Ala Ile Met Lys Glu Val His Gly Asn Asp Val Asp Gly Met Asp Leu
            20                  25                  30

Gly Lys Lys Val Ser Ile Pro Arg Asp Ile Met Leu Glu Glu Leu Ser
        35                  40                  45

His Leu Ser Asn Arg Gly Ala Arg Leu Phe Lys Met Arg Gln Arg Arg
    50                  55                  60

Ser Asp Lys Tyr Thr Phe Glu Asn Phe Gln Tyr Gln Ser Arg Ala Gln
65                  70                  75                  80

Ile Asn His Ser Ile Ala Met Gln Asn Gly Lys Val Asp Gly Ser Asn
                85                  90                  95

Leu Glu Gly Gly Ser Gln Gln Ala Pro Leu Thr Pro Pro Asn Thr Pro
            100                 105                 110

Asp Pro Arg Ser Pro Pro Asn Pro Asp Asn Ile Ala Pro Gly Tyr Ser
        115                 120                 125

Gly Pro Leu Lys Glu Ile Pro Pro Glu Lys Phe Asn Thr Thr Ala Val
    130                 135                 140

Pro Lys Tyr Tyr Gln Ser Pro Trp Glu Gln Ala Ile Ser Asn Asp Pro
145                 150                 155                 160
```

Glu Leu Leu Glu Ala Leu Tyr Pro Lys Leu Phe Lys Pro Glu Gly Lys
165 170 175

Ala Glu Leu Pro Asp Tyr Arg Ser Phe Asn Arg Val Ala Thr Pro Phe
180 185 190

Gly Gly Phe Glu Lys Ala Ser Arg Met Val Lys Phe Lys Val Pro Asp
195 200 205

Phe Glu Leu Leu Leu Leu Thr Asp Pro Arg Phe Met Ser Phe Val Asn
210 215 220

Pro Leu Ser Gly Arg Arg Ser Phe Asn Arg Thr Pro Lys Gly Trp Ile
225 230 235 240

Ser Glu Asn Ile Pro Ile Val Ile Thr Thr Glu Pro Thr Asp Asp Thr
245 250 255

Thr Val Pro Glu Ser Glu Asp Leu
260

<210> 3
<211> 1207
<212> DNA
<213> Mus musculus

<400> 3
gagagccgac caccaactga gcagctggtc agatccacct ccaccatgcc actctcagga 60
accccggccc ctaacaagag gaggaagtca agcaaactga ttatggagct cactggaggt 120
ggccgggaga gctcaggcct gaacctgggc aagaagatca gtgtcccaag ggatgtgatg 180
ttggaggagc tgtcccttct taccaaccga ggctccaaga tgttcaagct acggcagatg 240
cgggtggaga aatttatcta tgagaatcac cccgatgttt tctctgacag ctcaatggat 300
cacttccaga agtttcttcc cacagtggga ggacagctgg agacagctgg tcagggcttc 360
tcatatggca agggcagcag tggaggccag gctggcagca gtggctctgc tggacagtat 420
ggctctgacc gtcatcagca gggctctggg tttggagctg gggttcagg tggtcctggg 480
ggccaggctg gtggaggagg agctcctggc acagtagggc ttggagagcc cggatcaggt 540
gaccaggcag gtggagatgg aaaacatgtc actgtgttca agacttatat ttccccatgg 600
gatcgggcca tgggggttga tcctcagcaa aaagtggaac ttggcattga cctactggca 660
tacggtgcca aagctgaact ccccaaatat aagtccttca acaggacagc aatgccctac 720
ggtggatatg agaaggcctc caaacgcatg accttccaga tgcccaagtt tgacctgggg 780
cctctgctga gtgaacccct ggtcctctac aaccagaacc tctccaacag gccttctttc 840
aatcgaaccc ctattccctg gttgagctct ggggagcatg tagactacaa cgtggatgtt 900
ggtatcccct tggatggaga gacagaggag ctgtgaagtg cctcctcctg tcatgtgcat 960
catttccctt ctctggttcc aatttgagag tggatgctgg acaggatgcc ccaactgtta 1020
atccagtatt cttgtggcaa tggagggtaa agggtggggt ccgttgcctt tccacccttc 1080
aagttcctgc tccgaagcat ccctcctcac cagctcagag ctcccatcct gctgtaccat 1140
atggaatctg ctcttttatg gaattttctc tgccaccggt aacagtcaat aaacttcaag 1200
gaaatga 1207

<210> 4

<211> 296
<212> PRT
<213> Mus musculus

<400> 4

```
Met Pro Leu Ser Gly Thr Pro Ala Pro Asn Lys Arg Arg Lys Ser Ser
 1               5                  10                  15

Lys Leu Ile Met Glu Leu Thr Gly Gly Gly Arg Glu Ser Ser Gly Leu
            20                  25                  30

Asn Leu Gly Lys Lys Ile Ser Val Pro Arg Asp Val Met Leu Glu Glu
        35                  40                  45

Leu Ser Leu Leu Thr Asn Arg Gly Ser Lys Met Phe Lys Leu Arg Gln
    50                  55                  60

Met Arg Val Glu Lys Phe Ile Tyr Glu Asn His Pro Asp Val Phe Ser
65                  70                  75                  80

Asp Ser Ser Met Asp His Phe Gln Lys Phe Leu Pro Thr Val Gly Gly
                85                  90                  95

Gln Leu Glu Thr Ala Gly Gln Gly Phe Ser Tyr Gly Lys Gly Ser Ser
            100                 105                 110

Gly Gly Gln Ala Gly Ser Ser Gly Ser Ala Gly Gln Tyr Gly Ser Asp
        115                 120                 125

Arg His Gln Gln Gly Ser Gly Phe Gly Ala Gly Gly Ser Gly Gly Pro
    130                 135                 140

Gly Gly Gln Ala Gly Gly Gly Gly Ala Pro Gly Thr Val Gly Leu Gly
145                 150                 155                 160

Glu Pro Gly Ser Gly Asp Gln Ala Gly Gly Asp Gly Lys His Val Thr
                165                 170                 175

Val Phe Lys Thr Tyr Ile Ser Pro Trp Asp Arg Ala Met Gly Val Asp
            180                 185                 190

Pro Gln Gln Lys Val Glu Leu Gly Ile Asp Leu Leu Ala Tyr Gly Ala
        195                 200                 205

Lys Ala Glu Leu Pro Lys Tyr Lys Ser Phe Asn Arg Thr Ala Met Pro
    210                 215                 220

Tyr Gly Gly Tyr Glu Lys Ala Ser Lys Arg Met Thr Phe Gln Met Pro
225                 230                 235                 240

Lys Phe Asp Leu Gly Pro Leu Leu Ser Glu Pro Leu Val Leu Tyr Asn
                245                 250                 255
```

Gln Asn Leu Ser Asn Arg Pro Ser Phe Asn Arg Thr Pro Ile Pro Trp
260 265 270

Leu Ser Ser Gly Glu His Val Asp Tyr Asn Val Asp Val Gly Ile Pro
275 280 285

Leu Asp Gly Glu Thr Glu Glu Leu
290 295

<210> 5
<211> 1261
<212> DNA
<213> Homo sapiens

<400> 5
cggtcacagc agctcagtcc tccaaagctg ctggacccca gggagagctg accactgccc 60
gagcagccgg ctgaatccac ctccacaatg ccgctctcag gaaccccggc ccctaataag 120
aagaggaaat ccagcaagct gatcatggaa ctcactggag gtggacagga gagctcaggc 180
ttgaacctgg gcaaaaagat cagtgtccca agggatgtga tgttggagga actgtcgctg 240
cttaccaacc ggggctccaa gatgttcaaa ctgcggcaga tgagggtgga gaagtttatt 300
tatgagaacc accctgatgt tttctctgac agctcaatgg atcacttcca gaagttcctt 360
ccaacagtgg ggggacagct gggcacagct ggtcagggat tctcatacag caagagcaac 420
ggcagaggcg gcagccaggc aggggcagt ggctctgccg gacagtatgg ctctgatcag 480
cagcaccatc tgggctctgg gtctggagct gggggtacag gtggtcccgc gggccaggct 540
ggcaaaggag gagctgctgg cacaacaggg gttggtgaga caggatcagg agaccaggca 600
ggcggagaag gaaaacatat cactgtgttc aagacctata tttccccatg ggagcgagcc 660
atgggggttg acccccagca aaaaatggaa cttggcattg acctgctggc ctatggggcc 720
aaagctgaac ttcccaaata taagtccttc aacaggacgg caatgcccta tggtggatat 780
gagaaggcct ccaaacgcat gaccttccag atgcccaagt ttgacctggg gcccttgctg 840
agtgaacccc tggtcctcta caaccaaaac ctctccaaca ggccttcttt caatcgaacc 900
cctattccct ggctgagctc tggggagcct gtagactaca acgtggatat tggcatcccc 960
ttggatggag aaacagagga gctgtgaggt gtttcctcct ctgatttgca tcatttcccc 1020
tctctggctc caatttggag agggaatgct gagcagatag cccccattgt taatccagta 1080
tccttatggg aatggaggga aaaaggagag atctaccttt ccatccttta ctccaagtcc 1140
ccactccacg catccttcct caccaactca gagctcccct tctacttgct ccatatggaa 1200
cctgctcgtt tatggaattt ntctgccacc agtaacagtc aataaacttc aaggaaaatg 1260
a 1261

<210> 6
<211> 299
<212> PRT
<213> Homo sapiens

<400> 6
Met Pro Leu Ser Gly Thr Pro Ala Pro Asn Lys Lys Arg Lys Ser Ser
1 5 10 15

Lys Leu Ile Met Glu Leu Thr Gly Gly Gly Gln Glu Ser Ser Gly Leu
20 25 30

Asn Leu Gly Lys Lys Ile Ser Val Pro Arg Asp Val Met Leu Glu Glu

35 40 45

Leu Ser Leu Leu Thr Asn Arg Gly Ser Lys Met Phe Lys Leu Arg Gln
50 55 60

Met Arg Val Glu Lys Phe Ile Tyr Glu Asn His Pro Asp Val Phe Ser
65 70 75 80

Asp Ser Ser Met Asp His Phe Gln Lys Phe Leu Pro Thr Val Gly Gly
85 90 95

Gln Leu Gly Thr Ala Gly Gln Gly Phe Ser Tyr Ser Lys Ser Asn Gly
100 105 110

Arg Gly Gly Ser Gln Ala Gly Gly Ser Gly Ser Ala Gly Gln Tyr Gly
115 120 125

Ser Asp Gln Gln His His Leu Gly Ser Gly Ser Gly Ala Gly Gly Thr
130 135 140

Gly Gly Pro Ala Gly Gln Ala Gly Lys Gly Gly Ala Ala Gly Thr Thr
145 150 155 160

Gly Val Gly Glu Thr Gly Ser Gly Asp Gln Ala Gly Gly Glu Gly Lys
165 170 175

His Ile Thr Val Phe Lys Thr Tyr Ile Ser Pro Trp Glu Arg Ala Met
180 185 190

Gly Val Asp Pro Gln Gln Lys Met Glu Leu Gly Ile Asp Leu Leu Ala
195 200 205

Tyr Gly Ala Lys Ala Glu Leu Pro Lys Tyr Lys Ser Phe Asn Arg Thr
210 215 220

Ala Met Pro Tyr Gly Gly Tyr Glu Lys Ala Ser Lys Arg Met Thr Phe
225 230 235 240

Gln Met Pro Lys Phe Asp Leu Gly Pro Leu Leu Ser Glu Pro Leu Val
245 250 255

Leu Tyr Asn Gln Asn Leu Ser Asn Arg Pro Ser Phe Asn Arg Thr Pro
260 265 270

Ile Pro Trp Leu Ser Ser Gly Glu Pro Val Asp Tyr Asn Val Asp Ile
275 280 285

Gly Ile Pro Leu Asp Gly Glu Thr Glu Glu Leu
290 295

<210> 7
<211> 982

<212> DNA
<213> Mus musculus

<400> 7
attcggcaca tgggatcgag ggaccatgcc gttccaggtt caaggataaa acccattggg 60
ccatagtgcc gtcatattcc accttcagtg ccttcctcca caattgggat tcacccctgc 120
tgaaaagcgc acgctgacag caagggaaca aaaaactatg ctatcacata gtgccatggt 180
gaagcaaagg aaacagcaag catcagccat cacgaaggaa atccatggac atgatgttga 240
cggcatggac ctgggcaaaa aagttagcat ccccagagac atcatgatag aagaattgtc 300
ccatttcagt aatcgtgggg ccaggctgtt taagatgcgt caaagaagat ctgacaaata 360
cacctttgaa aatttccagt atgaatctag agcacaaatt aatcacaata tcgccatgca 420
gaatgggaga gttgatggaa gcaacctgga aggtggctca cagcaaggcc cctcaactcc 480
gcccaacacc cccgatccac gaagcccccc aaatccagag aacatcgcac caggatattc 540
tggaccactg aaggaaattc ctcctgaaag gtttaacacg acggccgttc ctaagtacta 600
ccggtctcca tgggagcagg cgattggcag cgatccggag ctcctggagg ctttgtaccc 660
aaaacttttc aagcctgaag gaaaagcaga actgcgggat tacaggagct ttaacagggt 720
tgccactcca tttggaggtt ttgaaaaagc atcaaaaatg gtcaaattca aagttccaga 780
ttttgaacta ctgctgctga cagatcccag gttcttggcc tttgccaatc ctctttcggg 840
cagacgatgc tttaacaggg cgccaaaggg gtgggtatct gagaatatcc ccgtcgtgat 900
cacaactgag cctacagaag acgccactgt accggaatca gatgacctgt gagagggaag 960
ctggggatgc cacaggaagt tc 982

<210> 8
<211> 264
<212> PRT
<213> Mus musculus

<400> 8
Met Leu Ser His Ser Ala Met Val Lys Gln Arg Lys Gln Gln Ala Ser
1 5 10 15

Ala Ile Thr Lys Glu Ile His Gly His Asp Val Asp Gly Met Asp Leu
20 25 30

Gly Lys Lys Val Ser Ile Pro Arg Asp Ile Met Ile Glu Glu Leu Ser
35 40 45

His Phe Ser Asn Arg Gly Ala Arg Leu Phe Lys Met Arg Gln Arg Arg
50 55 60

Ser Asp Lys Tyr Thr Phe Glu Asn Phe Gln Tyr Glu Ser Arg Ala Gln
65 70 75 80

Ile Asn His Asn Ile Ala Met Gln Asn Gly Arg Val Asp Gly Ser Asn
85 90 95

Leu Glu Gly Gly Ser Gln Gln Gly Pro Ser Thr Pro Pro Asn Thr Pro
100 105 110

Asp Pro Arg Ser Pro Pro Asn Pro Glu Asn Ile Ala Pro Gly Tyr Ser
115 120 125

Gly Pro Leu Lys Glu Ile Pro Pro Glu Arg Phe Asn Thr Thr Ala Val
    130   135   140

Pro Lys Tyr Tyr Arg Ser Pro Trp Glu Gln Ala Ile Gly Ser Asp Pro
145   150   155   160

Glu Leu Leu Glu Ala Leu Tyr Pro Lys Leu Phe Lys Pro Glu Gly Lys
                165   170   175

Ala Glu Leu Arg Asp Tyr Arg Ser Phe Asn Arg Val Ala Thr Pro Phe
            180   185   190

Gly Gly Phe Glu Lys Ala Ser Lys Met Val Lys Phe Lys Val Pro Asp
        195   200   205

Phe Glu Leu Leu Leu Leu Thr Asp Pro Arg Phe Leu Ala Phe Ala Asn
    210   215   220

Pro Leu Ser Gly Arg Arg Cys Phe Asn Arg Ala Pro Lys Gly Trp Val
225   230   235   240

Ser Glu Asn Ile Pro Val Val Ile Thr Thr Glu Pro Thr Glu Asp Ala
                245   250   255

Thr Val Pro Glu Ser Asp Asp Leu
            260

<210> 9
<211> 3330
<212> DNA
<213> Homo sapiens

<400> 9
gggacgccac gcaactctca gcttcccgac agaggtgtta atcttgaggg tctaagattc 60
cctcctgcct attgaggtcc catcctctca ggatgatccc caaggagcag aaggggccag 120
tgatggctgc catgggggac ctcactgaac cagtccctac gctggacctg ggcaagaagc 180
tgagcgtgcc ccaggacctg atgatggagg agctgtcact acgcaacaac agagggtccc 240
tcctcttcca gaagaggcag cgccgtgtgc agaagttcac tttcgagtta gcagccagcc 300
agcgggcgat gctggccgga agcgccagga ggaaggtgac tggaacagcg gagtcgggga 360
cggttgccaa tgccaatggc cctgaggggc cgaactaccg ctcggagctc cacatcttcc 420
cggcctcacc cggggcctca ctcgggggtc ccgagggcgc ccaccctgca gccgcccctg 480
ctgggtgcgt ccccagcccc agcgccctgg cgccaggcta tgcggagccg ctgaagggcg 540
tcccgccaga gaagttcaac cacaccgcca tccccaaggg ctaccgctgc ccttggcagg 600
agttcgtcag ctaccgggac taccagagcg atggccgaag tcacaccccc agccccaacg 660
actaccgaaa tttcaacaag accccggtgc catttggagg acccctcgtg gggggcactt 720
ttcccaggcc aggcaccccc ttcatcccgg agcccctcag tggcttggaa ctcctccgtc 780
tcagacccag cttcaacaga gtggcccagg gctgggtccg taacctccca gagtccgagg 840
agctgtagcc ctagcctgaa tcttcagttc cccagtctcg gggcctggt aacatccgga 900
gccaagactt gtggacagca cttcacagtt gaagaagggc cttcacacac aaaacctgat 960
tgcaaatggc ttcagaggtc accaagttca gtcgtcccaa aacatgggtg tgtttcaaaa 1020
ttacctgggg atgttgttcc aaatccagac aactggactg tcccagactt gcagcatcag 1080
agtctcctga gtcgaggaat ctgtattatt aatagcaacc agggccgggt gtcgtggctc 1140

acgcctgtca tcccagcact ttgggaggcc gaggcaggag gatcacctga ggtcaggagt 1200
tttgagacca gtctggccaa aatagtggaa ccccgtcgct actaaaaata caaaaatgag 1260
tcggacatgg tggtgcatgc ctgtaatccc agctacttgg gaggctgaga caggagaatc 1320
acttgaacta ggaggcagag gttgcagtga gccgagattg cgccactgca ccccagcctg 1380
gacaacagag tgagactcct tctcaaaagt aaataaataa atagcaacca gtactccagg 1440
tgattccagc ataacttatc catggtttgt gtcattagga gtccacatcc acacctctgc 1500
tctttcctgt tcctgtagtg tacactcccc cggtgacagg gtgctcactg gcaccccatc 1560
ttcctgtgaa taactcaaat aattagaaaa tgttcctttt actgagatgc agttggtctt 1620
catctattca tgctctaaac agttcctaag cgctgactgt gcgctagaca ctgccaggcc 1680
cgggcctcga ggaggaaaag acagtaggga agacattata gagcatgaag tcaccataat 1740
tttccctaaa gcatgcttat tgacaattga ggaacaaagt gttgggagca gaagaaggag 1800
tccctcaccc taggtgtgag atgggattct ggaagcttcc tgaaggattt gagtgggacc 1860
ttgtgggagg cgtgagagtc catgaagggg gtgtgagggg gagggtattt ctggaaagtg 1920
gaccagcatg tgcaaaaata tggaactgag cacgggtgca gggtgttctg cagaagggag 1980
aaggctgtgc tagaggagcc agtgagggcc agcatggggt gggcttcact aaggaaatgg 2040
ggaaggtttt agtgatgggt cttgctgggt gctgtgtggg gcgcatattg gagaagggta 2100
atgccagaag ccaggaagcc tgcaagggat gaggccatgg gaatggagag aaggggccac 2160
ccactgggca cctaacagga caggtgcaaa gtggggtgct tattaagatt ccttctttcc 2220
actccatttt gagcaggctg cttaaagtgg tggtgatgat gatgatgatg atggcagctt 2280
tatatcgagt gcctcagtgc ttgggctggt agtagtttct ctacatatct tatttctaat 2340
tctcagaaca accctgagag aaagatattg ttgtccccac tttacagatg tggatattta 2400
ggccaaaagg aggaagtgac tttccagggg cagacaccaa atgggaatct gattccagtg 2460
gatgtctctt ttcagtgcac tgggtggtca atgcccactc gctctgaaat catctgactg 2520
tgatgccctg ccttggagtt tagaagttga gtgcaggctt gggagtcaga ctggatgggg 2580
taggttctaa ctctgccact gctagccgga tgaacttgag caagtcattt cacatctccg 2640
agcctctgtt tctccaagtg taagatgagg acaagtataa aacctccttt atgggtttgt 2700
tgtgaacaca gtgcagggca catttataat aagagctcag tcaatggtag gtttcatgca 2760
actgctgctc taggctggaa aagttgttct tgcactggat gcagcatgag aagctggctg 2820
ctaagatgtc actgggggtc actaaagctg aagcctgaag gaaagcctct cattgctgta 2880
gagctctccc tgcctctctc tctggggcg atggggaagg tcaggagtcc agcccattcc 2940
cagggtgtgt gggatagcga ttgcatttc cttttgctct ggagtttcac tccccttctg 3000
ggtcccaagg gcccaatggc ctgactttta gaattgcttg caattggtgt tttctcttga 3060
atttgggggc tgccatttaa agccaggttt ccatgagctg aagaccagcc attcaagaat 3120
ctgaaaagta gacaagagga ctccagttgc ctcaggttgg ttctgctgtg ctctggaaag 3180
taactgcagc caccaggtat gaaaaggagc ctggtgggga gaccactgca cccaaaacaa 3240
atcctttctt cttctgagaa tgtgactttt tctggtgttg taaaaaagaa aaaaaaaaag 3300
aatgctcatt gtaaaaaaa aaaaaaaaaa 3330

<210> 10
<211> 251
<212> PRT
<213> Homo sapiens

<400> 10
Met Ile Pro Lys Glu Gln Lys Gly Pro Val Met Ala Ala Met Gly Asp
1 5 10 15

Leu Thr Glu Pro Val Pro Thr Leu Asp Leu Gly Lys Lys Leu Ser Val
20 25 30

Pro Gln Asp Leu Met Met Glu Glu Leu Ser Leu Arg Asn Asn Arg Gly
35 40 45

Ser Leu Leu Phe Gln Lys Arg Gln Arg Arg Val Gln Lys Phe Thr Phe
50 55 60

Glu Leu Ala Ala Ser Gln Arg Ala Met Leu Ala Gly Ser Ala Arg Arg
65 70 75 80

Lys Val Thr Gly Thr Ala Glu Ser Gly Thr Val Ala Asn Ala Asn Gly
85 90 95

Pro Glu Gly Pro Asn Tyr Arg Ser Glu Leu His Ile Phe Pro Ala Ser
100 105 110

Pro Gly Ala Ser Leu Gly Gly Pro Glu Gly Ala His Pro Ala Ala Ala
115 120 125

Pro Ala Gly Cys Val Pro Ser Pro Ser Ala Leu Ala Pro Gly Tyr Ala
130 135 140

Glu Pro Leu Lys Gly Val Pro Pro Glu Lys Phe Asn His Thr Ala Ile
145 150 155 160

Pro Lys Gly Tyr Arg Cys Pro Trp Gln Glu Phe Val Ser Tyr Arg Asp
165 170 175

Tyr Gln Ser Asp Gly Arg Ser His Thr Pro Ser Pro Asn Asp Tyr Arg
180 185 190

Asn Phe Asn Lys Thr Pro Val Pro Phe Gly Gly Pro Leu Val Gly Gly
195 200 205

Thr Phe Pro Arg Pro Gly Thr Pro Phe Ile Pro Glu Pro Leu Ser Gly
210 215 220

Leu Glu Leu Leu Arg Leu Arg Pro Ser Phe Asn Arg Val Ala Gln Gly
225 230 235 240

Trp Val Arg Asn Leu Pro Glu Ser Glu Glu Leu
245 250

<210> 11
<211> 913
<212> DNA
<213> Mus musculus

<400> 11
gtcggactgc aatagacaca caggccataa aactccagct tcccgactga agtgttaatc 60
ttgggggtct gacatttctt cccatctact gtggccccac caggatgatc cccaaggagc 120
agaaggagcc agtgatggct gtcccggggg accttgctga accagtccct tcgctggacc 180
tggggaagaa gctgagcgtg cctcaggacc taatgataga ggagctgtct ctacgaaaca 240
accgcggatc cctcctcttt cagaagaggc agcgccgggt gcagaagttt acctttgagc 300
tatcagaaag tttgcaggcc atcctggcga gtagtgcccg agggaaagtg gctggcagag 360

cggcgcaggc aacggttccc aatggcttgg aggagcagaa ccaccactcc gagacgcacg 420
tgttccaggg gtcacctggg gaccccggga tcacccatct gggagcagcg gggactgggt 480
cggtccgtag tccaagcgcc ctggcaccag gctatgcaga gcccctgaag ggcgtcccac 540
cggagaagtt caaccacact gccatcccca aaggctaccg gtgcccttgg caggagttca 600
ccagctacca agactactcg agtggcagca gaagtcacac tcccatcccc cgagactatc 660
gcaacttcaa caagaccccc gtgccatttg gaggacccca cgtgagggag gccattttcc 720
acgcaggcac cccctttgtc ccggagtcct tcagtggctt ggaacttctc cgcctcagac 780
ccaatttcaa cagggttgct cagggctggg tccggaagct cccggagtct gaggaactgt 840
agcctcagcc tgaagctaca attccctggg ctcaagaaac atgcttgtct tgaaaaaaaa 900
aaaaaaaaaa aaa 913

<210> 12
<211> 245
<212> PRT
<213> Mus musculus

<400> 12
Met Ile Pro Lys Glu Gln Lys Glu Pro Val Met Ala Val Pro Gly Asp
1 5 10 15

Leu Ala Glu Pro Val Pro Ser Leu Asp Leu Gly Lys Lys Leu Ser Val
20 25 30

Pro Gln Asp Leu Met Ile Glu Glu Leu Ser Leu Arg Asn Asn Arg Gly
35 40 45

Ser Leu Leu Phe Gln Lys Arg Gln Arg Arg Val Gln Lys Phe Thr Phe
50 55 60

Glu Leu Ser Glu Ser Leu Gln Ala Ile Leu Ala Ser Ser Ala Arg Gly
65 70 75 80

Lys Val Ala Gly Arg Ala Ala Gln Ala Thr Val Pro Asn Gly Leu Glu
85 90 95

Glu Gln Asn His His Ser Glu Thr His Val Phe Gln Gly Ser Pro Gly
100 105 110

Asp Pro Gly Ile Thr His Leu Gly Ala Ala Gly Thr Gly Ser Val Arg
115 120 125

Ser Pro Ser Ala Leu Ala Pro Gly Tyr Ala Glu Pro Leu Lys Gly Val
130 135 140

Pro Pro Glu Lys Phe Asn His Thr Ala Ile Pro Lys Gly Tyr Arg Cys
145 150 155 160

Pro Trp Gln Glu Phe Thr Ser Tyr Gln Asp Tyr Ser Ser Gly Ser Arg
165 170 175

Ser His Thr Pro Ile Pro Arg Asp Tyr Arg Asn Phe Asn Lys Thr Pro
180 185 190

```
Val Pro Phe Gly Gly Pro His Val Arg Glu Ala Ile Phe His Ala Gly
        195                 200                 205

Thr Pro Phe Val Pro Glu Ser Phe Ser Gly Leu Glu Leu Leu Arg Leu
    210                 215                 220

Arg Pro Asn Phe Asn Arg Val Ala Gln Gly Trp Val Arg Lys Leu Pro
225                 230                 235                 240

Glu Ser Glu Glu Leu
                245
```

human CAP-1

```
                                                          60
MLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVSIPRDIMLEELSHLSNRGARLFKM

                                                         120
RQRRSDKYTFENFQYQSRAQINHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNP

                                                         180
DNIAPGYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPKLFKPEGKAELP

                                                         240
DYRSFNRVATPFGGFEKASRMVKFKVPDFELLLLTDPRFMSFVNPLSGRRSFNRTPKGWI

SENIPIVITTEPTDDTTVPESEDL
```

FIG. 1A

mouse CAP-1

```
                                                          60
MLSHSAMVKQRKQQASAITKEIHGHDVDGMDLGKKVSIPRDIMIEELSHFSNRGARLFKM

                                                         120
RQRRSDKYTFENFQYESRAQINHNIAMQNGRVDGSNLEGGSQQGPSTPPNTPDPRSPPNP

                                                         180
ENIAPGYSGPLKEIPPERFNTTAVPKYYRSPWEQAIGSDPELLEALYPKLFKPEGKAELR

                                                         240
DYRSFNRVATPFGGFEKASKMVKFKVPDFELLLLTDPRFLAFANPLSGRRCFNRAPKGWV

SENIPVVITTEPTEDATVPESDDL
```

FIG. 1B

human CAP-2

```
                                                          60
MPLSGTPAPNKKRKSSKLIMELTGGGQESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF
                                                         120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
                                                         180
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGETGSGDQAGGEGKHITV
                                                         240
FKTYISPWERAMGVDPQQKMELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTF

QMPKFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEPVDYNVDIGIPLDGETEEL
```

FIG. 1C

mouse CAP-2

```
                                                          60
MPLSGTPAPNKRRKSSKLIMELTGGGRESSGLNLGKKISVPRDVMLEELSLLTNRGSKMF
                                                         120
KLRQMRVEKFIYENHPDVFSDSSMDHFQKFLPTVGGQLETAGQGFSYGKGSSGGQAGSSG
                                                         180
SAGQYGSDRHQQGSGFGAGGSGGPGGQAGGGGAPGTVGLGEPGSGDQAGGDGKHVTVFKT
                                                         240
YISPWDRAMGVDPQQKVELGIDLLAYGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMP

KFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWLSSGEHVDYNVDVGIPLDGETEEL
```

FIG. 1D

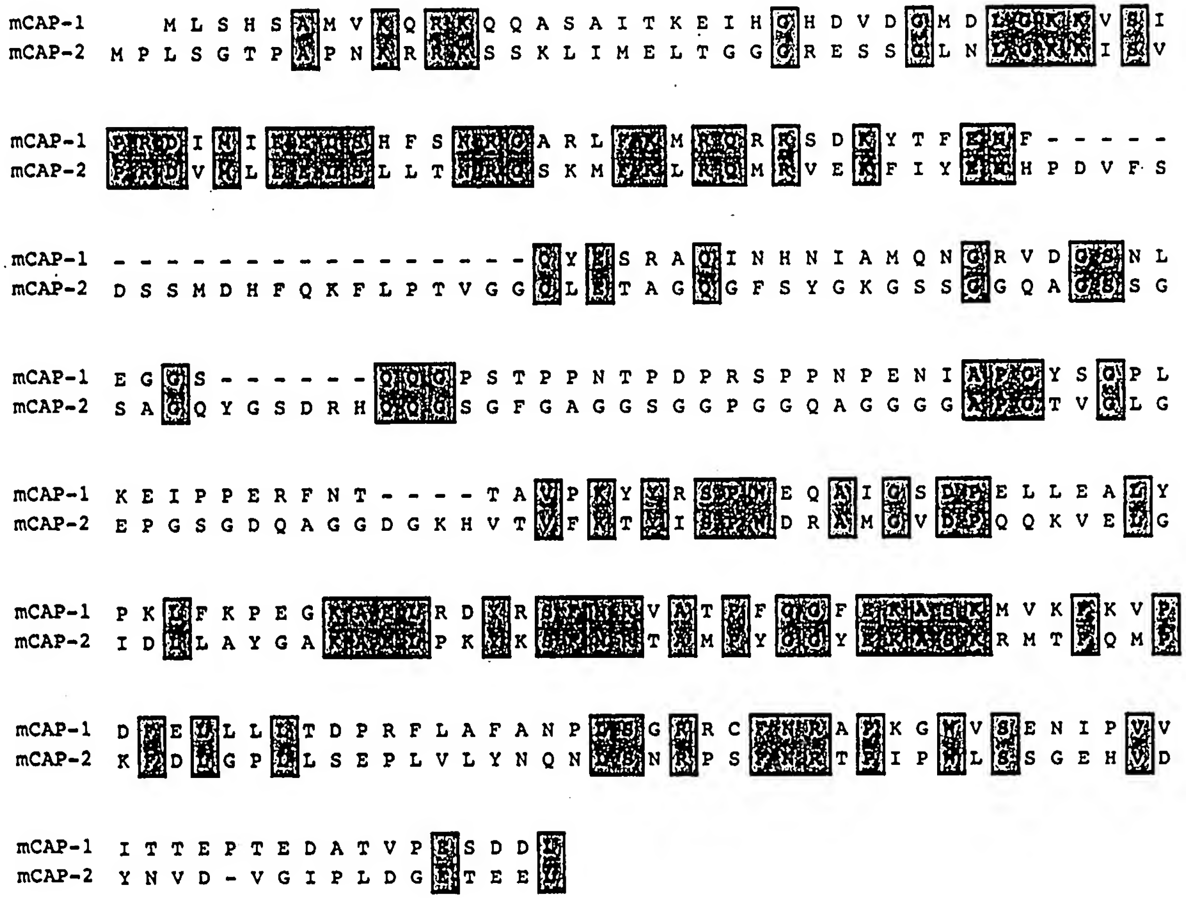


FIG. 1E

human CAP-1

```
        10        20        30        40        50        60        70        80        90       100
GTCCCAGGTTCAAGGATAAAAACCATCAGGCCCAAGTGCCATCCATAGTCCATCTCCAGAGTCTTCCTCCACAAACTGGGATTCATCCCCGCTGAAAAAG
CAGGGTCCAAGTTCCTATTTTTGGTAGTCCGGGTTCACGGTAGGTATCAGGTAGAGGTCTCAGAAGGAGGTGTTTGACCCTAAGTAGGGGCGACTTTTTC

       110       120       130       140       150       160       170       180       190       200
CACAATCTAACAGCAAGGGAACAAAAAAACCATGCTATCACATAATACTATGATGAAGCAGAGAAAACAGCAAGCAACAGCCATCATGAAGGAAGTCCAT
GTGTTAGATTGTCGTTCCCTTGTTTTTTTGGTACGATAGTGTATTATGATACTACTTCGTCTCTTTTGTCGTTCGTTGTCGGTAGTACTTCCTTCAGGTA

       210       220       230       240       250       260       270       280       290       300
GGAAATGATGTTGATGGCATGGACCTGGGCAAAAAGGTCAGCATCCCCAGAGACATCATGTTGGAAGAATTATCCCATCTCAGTAACCGTGGTGCCAGGC
CCTTTACTACAACTACCGTACCTGGACCCGTTTTTCCAGTCGTAGGGGTCTCTGTAGTACAACCTTCTTAATAGGGTAGAGTCATTGGCACCACGGTCCG

       310       320       330       340       350       360       370       380       390       400
TATTTAAGATGCGTCAAAGAAGATCTGACAAATACACATTTGAAAATTTCCAGTATCAATCTAGAGCACAAATAAATCACAGTATTGCTATGCAGAATGG
ATAAATTCTACGCAGTTTCTTCTAGACTGTTTATGTGTAAACTTTTAAAGGTCATAGTTAGATCTCGTGTTTATTTAGTGTCATAACGATACGTCTTACC

       410       420       430       440       450       460       470       480       490       500
GAAAGTGGATGGAAGTAACTTGGAAGGTGGTTCGCAGCAAGCCCCCTTGACTCCTCCCAACACCCCAGATCCACGAAGCCCTCCAAATCCAGACAACATT
CTTTCACCTACCTTCATTGAACCTTCCACCAAGCGTCGTTCGGGGGAACTGAGGAGGGTTGTGGGGTCTAGGTGCTTCGGGAGGTTTAGGTCTGTTGTAA

       510       520       530       540       550       560       570       580       590       600
GCTCCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAAATTCAACACCACAGCTGTCCCTAAGTACTATCAATCTCCCTGGGAGCAAGCCATTA
CGAGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTTTAAGTTGTGGTGTCGACAGGGATTCATGATAGTTAGAGGGACCCTCGTTCGGTAAT

       610       620       630       640       650       660       670       680       690       700
GCAATGATCCGGAGCTTTTAGAGGCTTTATATCCTAAACTTTTCAAGCCTGAAGGAAAGGCAGAACTGCCTGATTACAGGAGCTTTAACAGGGTTGCCAC
CGTTACTAGGCCTCGAAAATCTCCGAAATATAGGATTTGAAAAGTTCGGACTTCCTTTCCGTCTTGACGGACTAATGTCCTCGAAATTGTCCCAACGGTG

       710       720       730       740       750       760       770       780       790       800
ACCATTTGGAGGTTTTGAAAAAGCATCAAGAATGGTTAAATTTAAAGTTCCAGATTTTGAGCTACTATTGCTAACAGATCCCAGGTTTATGTCCTTTGTC
TGGTAAACCTCCAAAACTTTTTCGTAGTTCTTACCAATTTAAATTTCAAGGTCTAAAACTCGATGATAACGATTGTCTAGGGTCCAAATACAGGAAACAG

       810       820       830       840       850       860       870       880       890       900
AATCCCCTTTCTGGCAGACGGTCCTTTAATAGGACTCCTAAGGGATGGATATCTGAGAATATTCCTATAGTGATAACAACCGAACCTACAGATGATACCA
TTAGGGGAAAGACCGTCTGCCAGGAAATTATCCTGAGGATTCCCTACCTATAGACTCTTATAAGGATATCACTATTGTTGGCTTGGATGTCTACTATGGT

       910       920       930       940       950       960       970       980       990      1000
CTGTACCAGAATCAGAAGACCTATGAAAAGAAAGTTGTATGTGCCACATAAAACTCTGAATATAAAAGTTGCTGTTCTACTATTTTAACTACTGGCAAAG
GACATGGTCTTAGTCTTCTGGATACTTTTCTTTCAACATACACGGTGTATTTTGAGACTTATATTTTCAACGACAAGATGATAAAATTGATGACCGTTTC

      1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
CACTTGCATTTTTCATTAGTAGCAACAATAGCAATTTAGTGATTTTCCTTTTCTGACATTCAATTTCAATCTCAGATCAAATACTAATAAACAATTAGAA
GTGAACGTAAAAAGTAATCATCGTTGTTATCGTTAAATCACTAAAAGGAAAAGACTGTAAGTTAAAGTTAGAGTCTAGTTTATGATTATTTGTTAATCTT

      1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
ATCTTACTTTAAAAAACTTATAACTCACTTGTCTTCATTCATAATTTTGTTTTCACCTGGTTTAAAGAATCCAGATATTTTACTGCAAAAGTTCAGATGG
TAGAATGAAATTTTTTGAATATTGAGTGAACAGAAGTAAGTATTAAAACAAAAGTGGACCAAATTTCTTAGGTCTATAAAATGACGTTTTCAAGTCTACC

      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
AAAAGTAATTGACAGCTTCACCTTTGTCTCATTTTATATGATTTATTACAGTGTAAGTTTTTCAAGTGGAATCTAGAATCAAAATACAGGGAGAGATATG
TTTTCATTAACTGTCGAAGTGGAAACAGAGTAAAATATACTAAATAATGTCACATTCAAAAAGTTCACCTTAGATCTTAGTTTTATGTCCCTCTCTATAC

      1310      1320      1330      1340      1350      1360      1370      1380      1390      1400
AAGACCTATTCAGAGTTTCATCTGGGGATGAAAGCTATGGAAGATGATGTACAAATGTTATTGATGGAGAAAATGGTTGGTGTGTCCTTTCTGGTGACCA
TTCTGGATAAGTCTCAAAGTAGACCCCTACTTTCGATACCTTCTACTACATGTTTACAATAACTACCTCTTTTACCAACCACACAGGAAAGACCACTGGT

      1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
TGAGAAAATAATATGTCTTGATGAAGTCTTTTCATTAGTCACTCTTAGAATTCTAAAGTGCTTTGCACTTTTCAATATGTTTTGAATCATTAGGTAATTT
ACTCTTTTATTATACAGAACTACTTCAGAAAAGTAATCAGTGAGAATCTTAAGATTTCACGAAACGTGAAAAGTTATACAAAACTTAGTAATCCATTAAA

      1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
ATTCTGGATGATATTCTCCAAAATTCAATTCAGTTATTATATTCATTTAGCATTAAGTCAAGGAGACTGAGAATGACTCAAGGGACGTCATAGTACCATA
TAAGACCTACTATAAGAGGTTTTAAGTTAAGTCAATAATATAAGTAAATCGTAATTCAGTTCCTCTGACTCTTACTGAGTTCCCTGCAGTATCATGGTAT

      1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
GTTTTAAGGACCAAGGTGTGCCCAGAATTCAAGTTTCACAAATCCCAATGCTGTGCATTGATTATGTTCAACTTTATGTGTGCATTCTTAGAAGAGTAAG
CAAAATTCCTGGTTCCACACGGGTCTTAAGTTCAAAGTGTTTAGGGTTACGACACGTAACTAATACAAGTTGAAATACACACGTAAGAATCTTCTCATTC

      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
AACAAATAAAGTACACCGTAATATACATATAAATACATTCATGTTTGTGAGAGAAGGAAAGAGTAAGTAATTTGAATTGGCAGCTTTCTTTGCTAAATCT
TTGTTTATTTCATGTGGCATTATATGTATATTTATGTAAGTACAAACACTCTCTTCCTTTCTCATTCATTAAACTTAACCGTCGAAAGAAACGATTTAGA

      1810      1820      1830      1840      1850      1860      1870      1880      1890      1900
TTAAATTCTGTTAAGATCCTCAAGTAACTGGGGAGTACATGCTTTAGGACACAAACAAAAACAAAGGGCATGAAAGTATCTGAAAGCAATGTAGCACATA
AATTTAAGACAATTCTAGGAGTTCATTGACCCCTCATGTACGAAATCCTGTGTTTGTTTTTGTTTCCCGTACTTTCATAGACTTTCGTTACATCGTGTAT

      1910      1920      1930      1940      1950      1960      1970      1980      1990      2000
TCTATCGTAATATATGTAATATATTGACATAAAAGACACAAACTAATATAAAGTTATAGTTATATCTTAAAATATAATTGAAGAAGCATATGACATATAA
AGATAGCATTATATACATTATATAACTGTATTTTCTGTGTTTGATTATATTTCAATATCAATATAGAATTTTATATTAACTTCTTCGTATACTGTATATT

      2010      2020      2030      2040      2050      2060      2070      2080      2090      2100
CTTATAGAAATCAGTATCAATTCCTCCCATTTCAATTCAGTTAAGACTTCTGTGATAGATGTTTATAGCAGAGAAGAAATGTCTCATCAATAGGAAAACT
GAATATCTTTAGTCATAGTTAAGGAGGGTAAAGTTAAGTCAATTCTGAAGACACTATCTACAAATATCGTCTCTTCTTTACAGAGTAGTTATCCTTTTGA

      2110      2120      2130      2140      2150      2160      2170      2180      2190      2200
ATCAGATAAAGTTTAGGAGATAGGAAGAAGGACTGTGTGTAGTAATGAAAATACCAAGTTGCAACATTACATGTTTACAAAAAAAATCTGTGTTTGTAGT
TAGTCTATTTCAAATCCTCTATCCTTCTTCCTGACACACATCATTACTTTTATGGTTCAACGTTGTAATGTACAAATGTTTTTTTTAGACACAAACATCA

      2210      2220      2230      2240      2250      2260      2270      2280      2290      2300
GTGGAAGTTGGTGACTGTTTTAATCATCATCTAGACTTGTTAAGTAGAAAAATTTTAAAAATTTGCTTATGAAAATATAACCCCCAGAAAGTAACAATGA
CACCTTCAACCACTGACAAAATTAGTAGTAGATCTGAACAATTCATCTTTTTAAAATTTTTAAACGAATACTTTTATATTGGGGGTCTTTCATTGTTACT

      2310      2320      2330      2340      2350      2360      2370      2380      2390      2400
CAAAGTATTATATTTATATATATTATTGTAGAGAATTTGTATATTTTTAAAGATGTCTTAAGATATCTTAATTTTATTTATAAGTTTTGGTGTTTACCTG
GTTTCATAATATAAATATATATAATAACATCTCTTAAACATATAAAAATTTCTACAGAATTCTATAGAATTAAAATAAATATTCAAAACCACAAATGGAC

      2410      2420      2430      2440      2450      2460      2470      2480      2490      2500
TTTTAAAATGATAATGTTGGCATCTGTGATAAACTATCAATGAGGCTCCCATCATGCCATTTTTTGTTCATTTTAATCTTTAAAAAATAAAAATTAGGCA
AAAATTTTACTATTACAACCGTAGACACTATTTGATAGTTACTCCGAGGGTAGTACGGTAAAAAACAAGTAAAATTAGAAATTTTTTATTTTTAATCCGT

      2510      2520      2530
TATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ATAATTTTTTTTTTTTTTTTTTTTTTTTTTTT
```

FIG. 2A

mouse CAP-1

```
        10        20        30        40        50        60        70        80        90       100
ATTCGGCACATGGGATCGAGGGACCATGCCGTTCCAGGTTCAAGGATAAAACCCATTGGGCCATAGTGCCGTCATATTCCACCTTCAGTGCCTTCCTCCA
TAAGCCGTGTACCCTAGCTCCCTGGTACGGCAAGGTCCAAGTTCCTATTTTGGGTAACCCGGTATCACGGCAGTATAAGGTGGAAGTCACGGAAGGAGGT

       110       120       130       140       150       160       170       180       190       200
CAATTGGGATTCACCCCTGCTGAAAAGCGCACGCTGACAGCAAGGGAACAAAAAACTATGCTATCACATAGTGCCATGGTGAAGCAAAGGAAACAGCAAG
GTTAACCCTAAGTGGGGACGACTTTTCGCGTGCGACTGTCGTTCCCTTGTTTTTTGATACGATAGTGTATCACGGTACCACTTCGTTTCCTTTGTCGTTC

       210       220       230       240       250       260       270       280       290       300
CATCAGCCATCACGAAGGAAATCCATGGACATGATGTTGACGGCATGGACCTGGGCAAAAAAGTTAGCATCCCCAGAGACATCATGATAGAAGAATTGTC
GTAGTCGGTAGTGCTTCCTTTAGGTACCTGTACTACAACTGCCGTACCTGGACCCGTTTTTTCAATCGTAGGGGTCTCTGTAGTACTATCTTCTTAACAG

       310       320       330       340       350       360       370       380       390       400
CCATTTCAGTAATCGTGGGGCCAGGCTGTTTAAGATGCGTCAAAGAAGATCTGACAAATACACCTTTGAAAATTTCCAGTATGAATCTAGAGCACAAATT
GGTAAAGTCATTAGCACCCCGGTCCGACAAATTCTACGCAGTTTCTTCTAGACTGTTTATGTGGAAACTTTTAAAGGTCATACTTAGATCTCGTGTTTAA

       410       420       430       440       450       460       470       480       490       500
AATCACAATATCGCCATGCAGAATGGGAGAGTTGATGGAAGCAACCTGGAAGGTGGCTCACAGCAAGGCCCCTCAACTCCGCCCAACACCCCCGATCCAC
TTAGTGTTATAGCGGTACGTCTTACCCTCTCAACTACCTTCGTTGGACCTTCCACCGAGTGTCGTTCCGGGGAGTTGAGGCGGGTTGTGGGGGCTAGGTG

       510       520       530       540       550       560       570       580       590       600
GAAGCCCCCCAAATCCAGAGAACATCGCACCAGGATATTCTGGACCACTGAAGGAAATTCCTCCTGAAAGGTTTAACACGACGGCCGTTCCTAAGTACTA
CTTCGGGGGGTTTAGGTCTCTTGTAGCGTGGTCCTATAAGACCTGGTGACTTCCTTTAAGGAGGACTTTCCAAATTGTGCTGCCGGCAAGGATTCATGAT

       610       620       630       640       650       660       670       680       690       700
CCGGTCTCCATGGGAGCAGGCGATTGGCAGCGATCCGGAGCTCCTGGAGGCTTTGTACCCAAAACTTTTCAAGCCTGAAGGAAAAGCAGAACTGCGGGAT
GGCCAGAGGTACCCTCGTCCGCTAACCGTCGCTAGGCCTCGAGGACCTCCGAAACATGGGTTTTGAAAAGTTCGGACTTCCTTTTCGTCTTGACGCCCTA

       710       720       730       740       750       760       770       780       790       800
TACAGGAGCTTTAACAGGGTTGCCACTCCATTTGGAGGTTTTGAAAAAGCATCAAAAATGGTCAAATTCAAAGTTCCAGATTTTGAACTACTGCTGCTGA
ATGTCCTCGAAATTGTCCCAACGGTGAGGTAAACCTCCAAAACTTTTTCGTAGTTTTTACCAGTTTAAGTTTCAAGGTCTAAAACTTGATGACGACGACT

       810       820       830       840       850       860       870       880       890       900
CAGATCCCAGGTTCTTGGCCTTTGCCAATCCTCTTTCGGGCAGACGATGCTTTAACAGGGCGCCAAAGGGGTGGGTATCTGAGAATATCCCCGTCGTGAT
GTCTAGGGTCCAAGAACCGGAAACGGTTAGGAGAAAGCCCGTCTGCTACGAAATTGTCCCGCGGTTTCCCCACCCATAGACTCTTATAGGGGCAGCACTA

       910       920       930       940       950       960       970       980
CACAACTGAGCCTACAGAAGACGCCACTGTACCGGAATCAGATGACCTGTGAGAGGGAAGCTGGGGATGCCACAGGAAGTTC
GTGTTGACTCGGATGTCTTCTGCGGTGACATGGCCTTAGTCTACTGGACACTCTCCCTTCGACCCCTACGGTGTCCTTCAAG
```

FIG. 2B

human CAP-2

100
CGGTCACAGC AGCTCAGTCC TCCAAAGCTG CTGGACCCCA GGGAGAGCTG ACCACTGCCC GAGCAGCCGG CTGAATCCAC CTCCACAATG CCGCTCTCAG

200
GAACCCCGGC CCCTAATAAG AAGAGGAAAT CCAGCAAGCT GATCATGGAA CTCACTGGAG GTGGACAGGA GAGCTCAGGC TTGAACCTGG GCAAAAAGAT

300
CAGTGTCCCA AGGGATGTGA TGTTGGAGGA ACTGTCGCTG CTTACCAACC GGGGCTCCAA GATGTTCAAA CTGCGGCAGA TGAGGGTGGA GAAGTTTATT

400
TATGAGAACC ACCCTGATGT TTTCTCTGAC AGCTCAATGG ATCACTTCCA GAAGTTCCTT CCAACAGTGG GGGGACAGCT GGGCACAGCT GGTCAGGGAT

500
TCTCATACAG CAAGAGCAAC GGCAGAGGCG GCAGCCAGGC AGGGGGCAGT GGCTCTGCCG GACAGTATGG CTCTGATCAG CAGCACCATC TGGGCTCTGG

600
GTCTGGAGCT GGGGGTACAG GTGGTCCCGC GGGCCAGGCT GGCAGAGGAG GAGCTGCTGG CACACAGGGG GTTGGTGAGA CAGGATCAGG AGACCAGGCA

700
GGCGGAGAAG GAAAACATAT CACTGTGTTC AAGACCTATA TTTCCCCATG GGAGCGAGCC ATGGGGGTTG ACCCCCAGCA AAAAATGGAA CTTGGCATTG

800
ACCTGCTGGC CTATGGGGCC AAAGCTGAAC TTCCCAAATA TAAGTCCTTC AACAGGACGG CAATGCCCTA TGGTGGATAT GAGAAGGCCT CCAAACGCAT

900
GACCTTCCAG ATGCCCAAGT TTGACCTGGG GCCCTTGCTG AGTGAACCCC TGGTCCTCTA CAACCAAAAC CTCTCCAACA GGCCTTCTTT CAATCGAACC

1000
CCTATTCCCT GGCTGAGCTC TGGGGAGCCT GTAGACTACA ACGTGGATAT TGGCATCCCC TTGGATGGAG AAACAGAGGA GCTGTGAGGT GTTTCCTCCT

CTGATTTGCA TCATTTCCCC TCTCTGGCTC CAATTTGGAG A

FIG. 2C

mouse CAP-2

```
                                                                                                    100
GCCGGGGAGA GCCGACCACC AACTGAGCAG CTGGTCAGAT CCACCTCCAC CATGCCACGC TCAGGAACCC CGGCCCCTAA CAAGAGGAGG AAGTCAAGCA
                                                                                                    200
AACTGATTAT GGAGCTCACT GGAGGTGGCC GGGAGAGCTC AGGCCTGAAC CTGGGCAAGA AGATCAGTGT CCCAAGGGAT GTGATGTTGG AGGAGCTGTC
                                                                                                    300
CCTTCTTACC AACCGAGGCT CCAAGATGTT CAAGCTACGG CAGATGCGGG TGGAGAAATT TATCTATGAG AATCACCCCG ATGTTTTCTC TGACAGCTCA
                                                                                                    400
ATGGATCACT TCCAGAAGTT TCTTCCCACA GTGGGAGGAC AGCTGGAGAC AGCTGGTCAG GGCTTCTCAT ATGGCAAGGG CAGCAGTGGA GGCCAGGCTG
                                                                                                    500
GCAGCAGTGG CTCTGCTGGA CAGTATGGCT CTGACCGTCA TCAGCAGGGC TCTGGGTTTG GAGCTGGGGG TTCAGGTGGT CCTGGGGGCC AGGCTGGTGG
                                                                                                    600
AGGAGGAGCT CCTGGCACAG TAGGGCTTGG AGAGCCCGGA TCAGGTGACC AGGCAGGTGG AGATGGAAAA CATGTCACTG TGTTCAAGAC TTATATTTCC
                                                                                                    700
CCATGGGATC GGGCCATGGG GGTTGATCCT CAGCAAAAAG TGGAACTTGG CATTGACCTA CTGGCATACG GTGCCAAAGC TGAACTCCCC AAATATAAGT
                                                                                                    800
CCTTCAACAG GACAGCAATG CCCTACGGTG GATATGAGAA GGCCTCCAAA CGCATGACCT TCCAGATGCC CAAGTTTGAC CTGGGGCCTC TGCTGAGTGA
                                                                                                    900
ACCCCTGGTC CTCTACAACC AGAACCTCTC CAACAGGCCT TCTTTCAATC GAACCCCTAT TCCCTGGTTG AGCTCTGGGG AGCATGTAGA CTACAACGTG
                                                                                                   1000
GATGTTGGTA TCCCCTTGGA TGGAGAGACA GAGGAGCTGT GAAGTGCCTC CTCCTGTCAT GTGCATCATT TCCCTTCTCT GGTTCCAATT TGAGAGTGGA
                                                                                                   1100
TGCTGGACAG GATGCCCCAA CTGTTAATCC AGTATTCTTG TGGCAATGGA GGGTAAAGGG TGGGGTCCGT TGCCTTTCCA CCCTTCAAGT TCCTGCTCCG
AAGCATCCCT CCTCACCAGC TCAGAGCTCC CATCCTGCTG TACCATATGG AATCTGCTCT TTTATGGAAT TTTCT
```

FIG. 2D

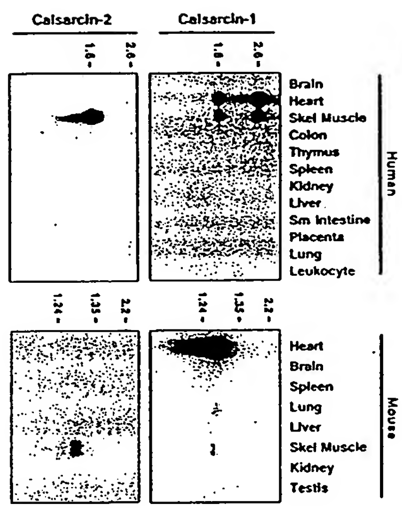

Calsarcin-2
Calsarcin-1
1.6-
2.6-
1.8-
2.6-
Brain
Heart
Skel Muscle
Colon
Thymus
Spleen
Kidney
Liver
Sm Intestine
Placenta
Lung
Leukocyte
Human
1.24-
1.35-
2.2-
1.24-
1.33-
2.2-
Heart
Brain
Spleen
Lung
Liver
Skel Muscle
Kidney
Testis
Mouse

FIG. 3

FIG. 4A

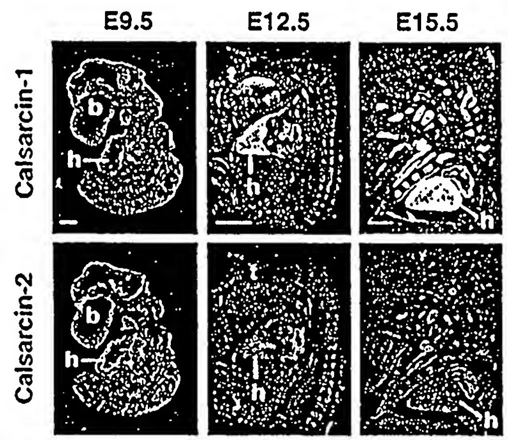


FIG. 4C

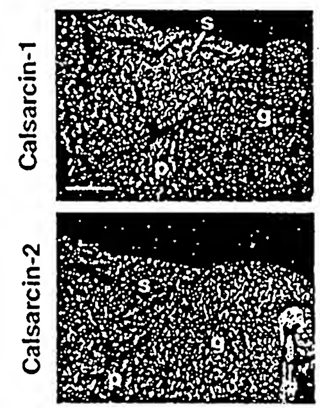


FIG. 4B

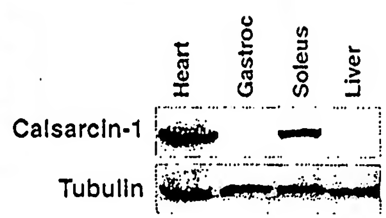


FIG. 4D

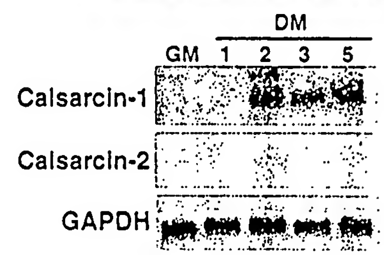


FIG. 4E

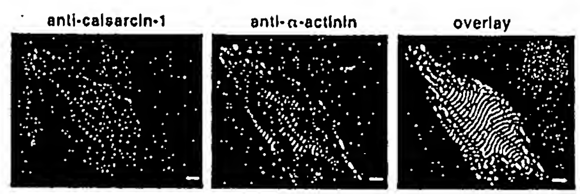

anti-calsarcin-1
anti-α-actinin
overlay

FIG. 5A


anti-calsarcin-1
anti-calcineurin
overlay

FIG. 5B

FIG. 6A

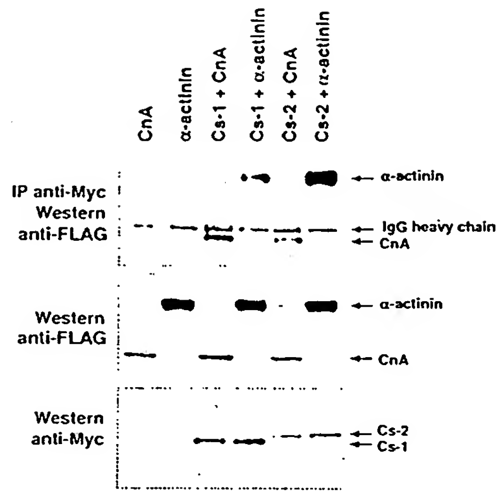


FIG. 6B

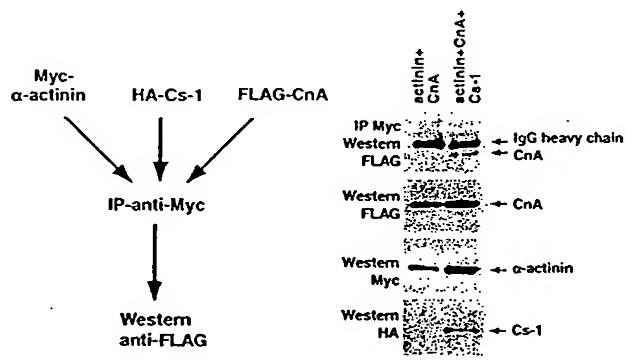
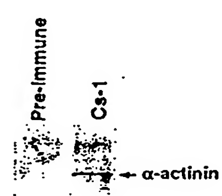


FIG. 6C



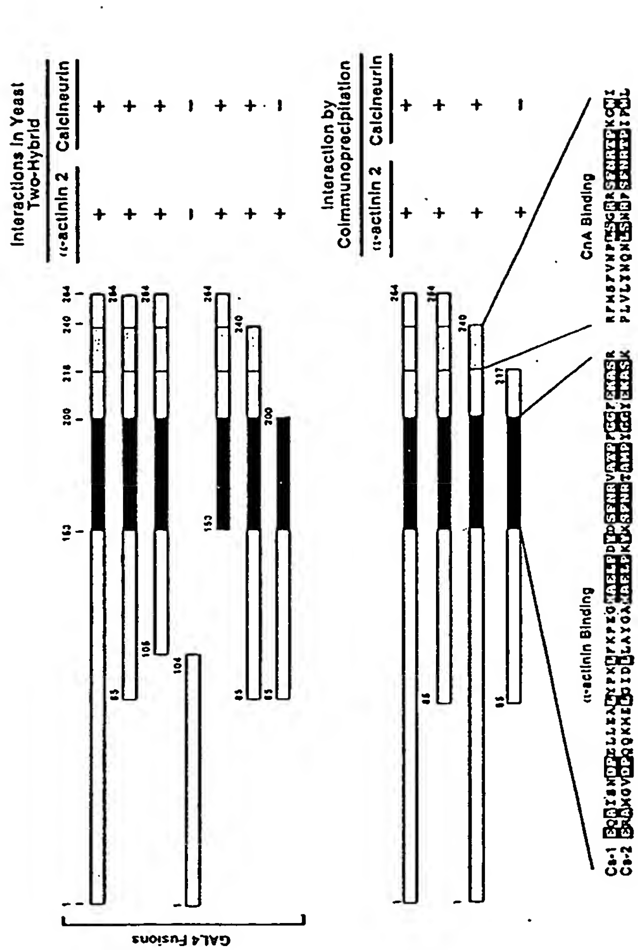

Interactions in Yeast Two-Hybrid
α-actinin 2
Calcineurin
Interaction by Coimmunoprecipitation
α-actinin 2
Calcineurin
GAL4 Fusions
α-actinin Binding
CnA Binding

FIG. 7

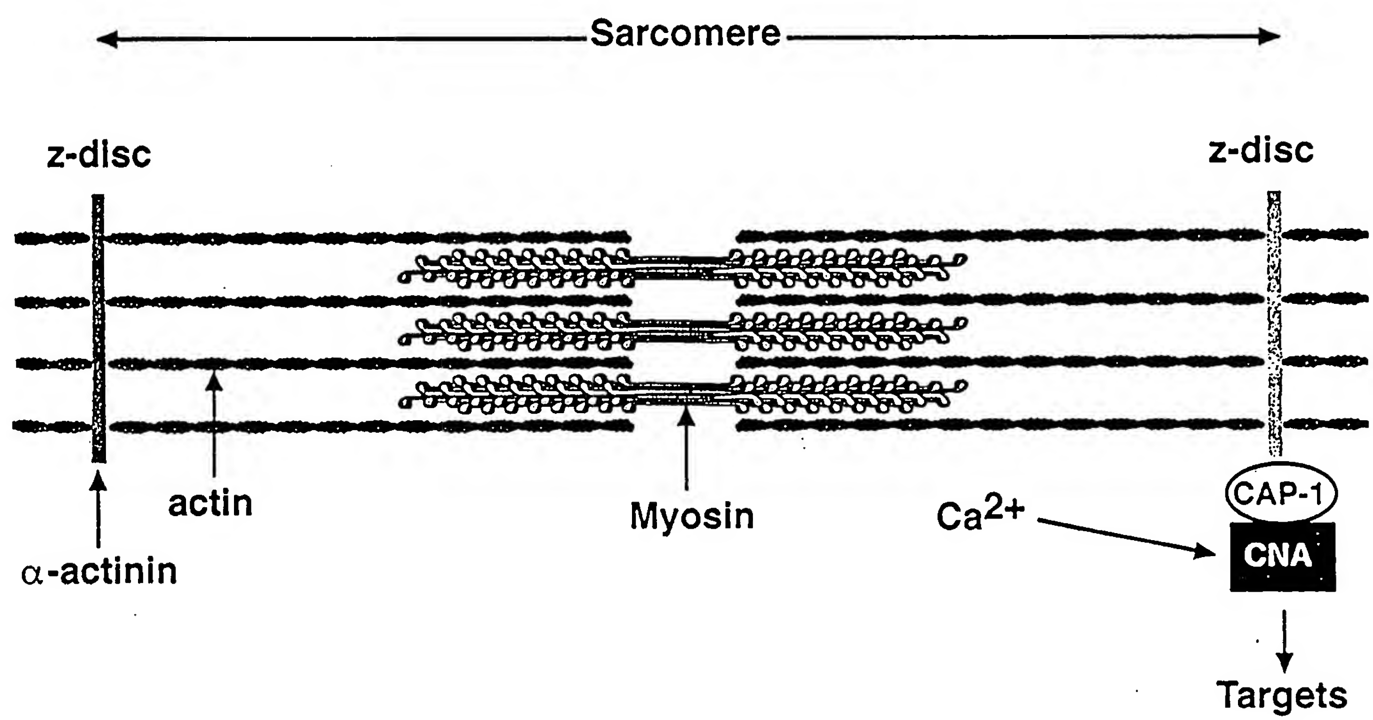
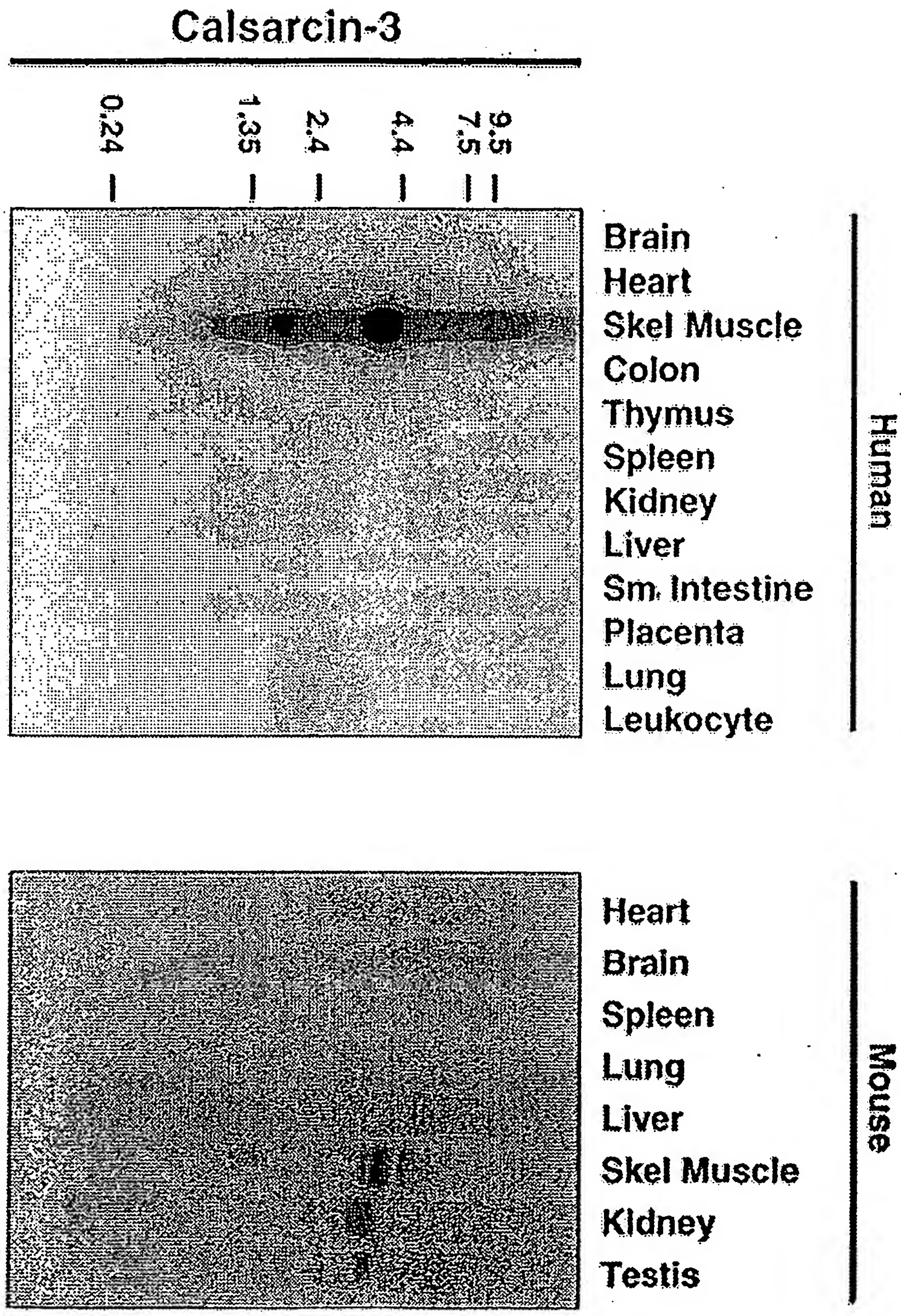
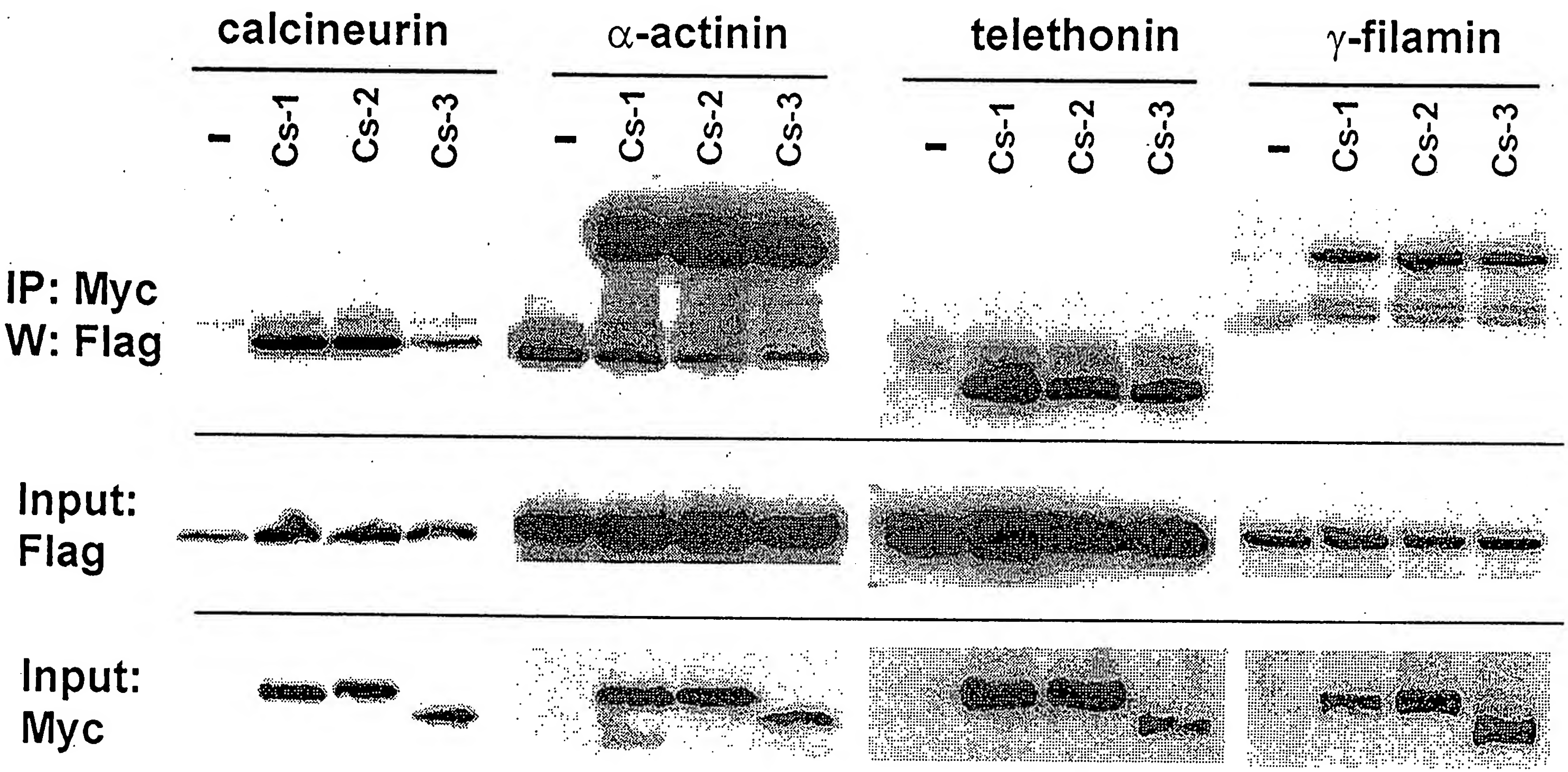

Sarcomere
z-disc
z-disc
actin
α-actinin
Myosin
Ca2+
CAP-1
CNA
Targets

FIG. 8



BEST AVAILABLE COPY

FIG. 9



calcineurin
α-actinin
telethonin
γ-filamin
-
Cs-1
Cs-2
Cs-3
IP: Myc
W: Flag
Input:
Flag
Input:
Myc

FIG. 10

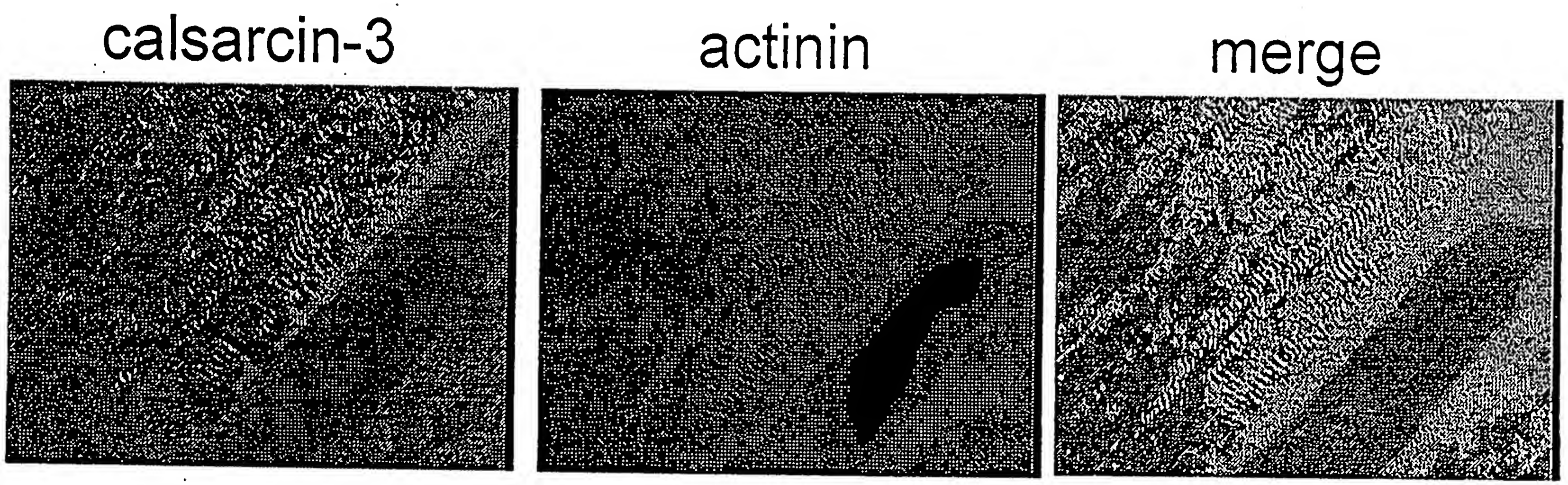
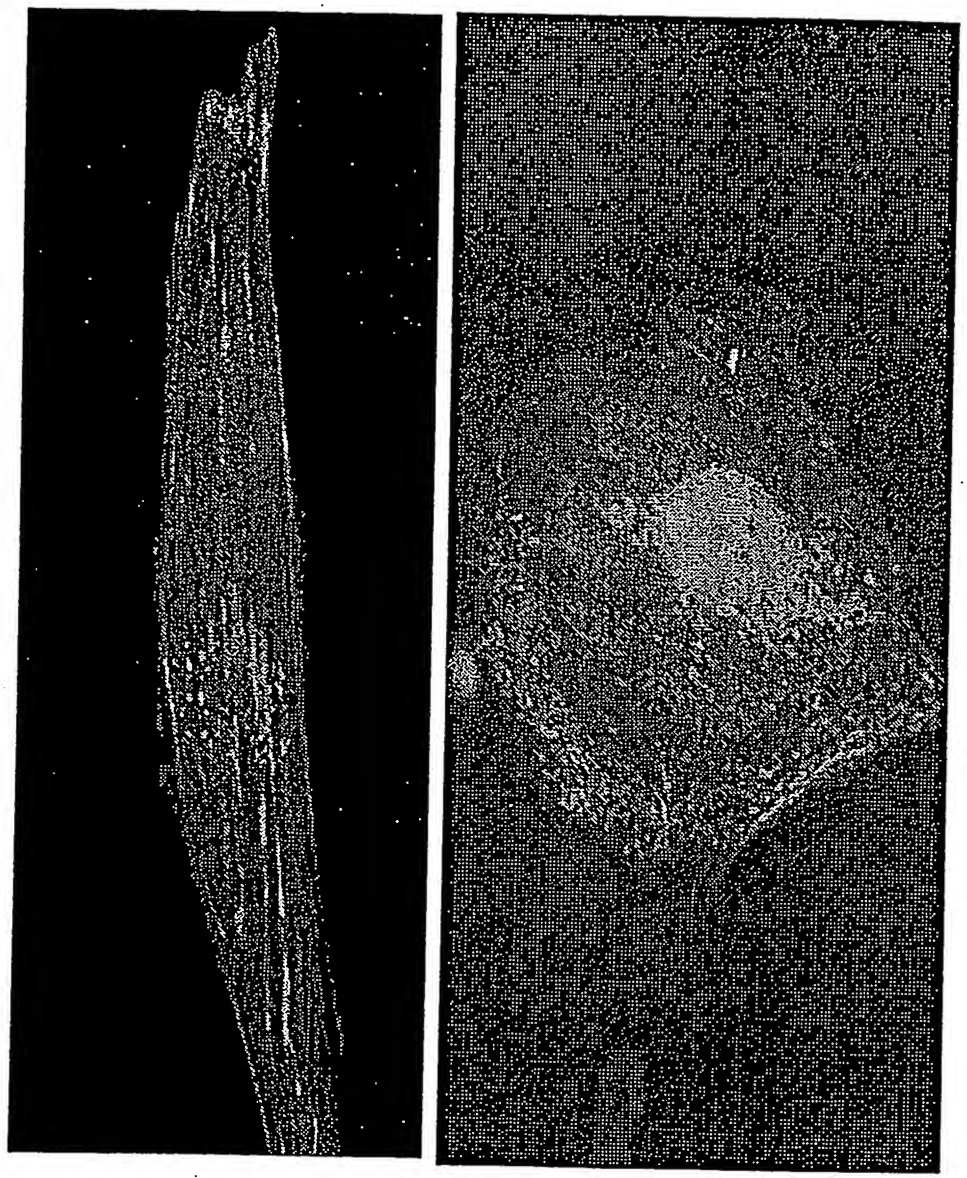


FIG. 11

FIG. 12



ClustalW Formatted Alignments

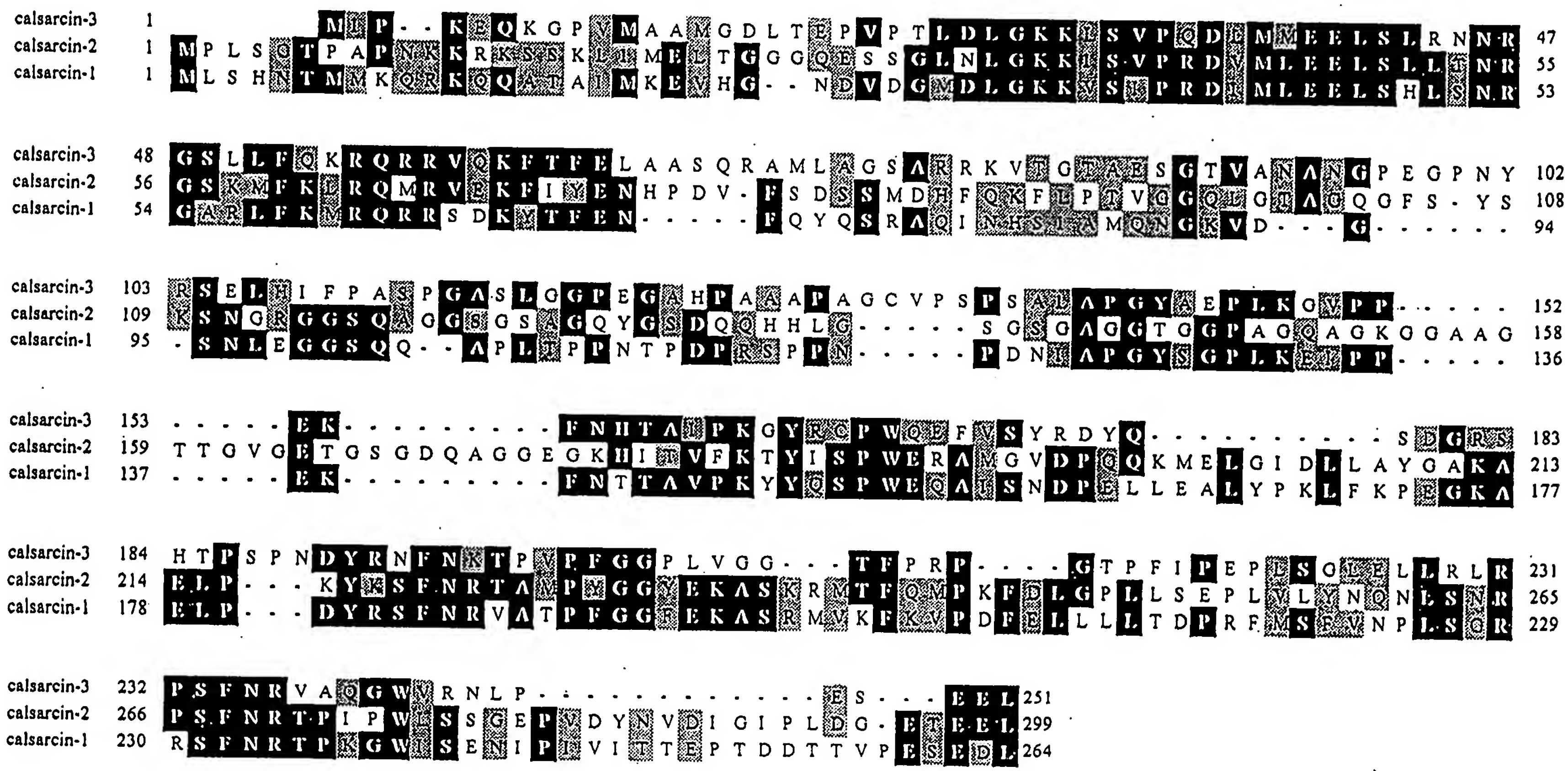


FIG. 13